

AMENDMENTS TO THE SPECIFICATION

Please amend the first paragraph of the Specification as follows:

CROSS-REFERENCE TO RELATED APPLICATION(S)

This application is a Section 371 National Stage Application of International No. PCT/FR2005/000070, filed 12 January 2005 and published as WO 2005/073364 A1 on 11 August 2005, which claims priority from the France Application 0400214, filed 12 January 2004, the subject matter of which are hereby incorporated by reference in its entirety.

Please replace the paragraph at page 7, lines 13-20 with the following amended paragraph.

The means of identification of the homologous sequences and their percentage homologies are well-known to those skilled in the art, and include in particular the BLAST programmes that can be used on the website <http://www.ncbi.nlm.nih.gov/BLAST/> with the default parameters indicated on that website. The sequences obtained can be exploited (aligned) using for example the programmes CLUSTALW (<http://www.ebi.ac.uk/clustalw/>) or MULTALIN (<http://prodes.toulouse.inra.fr/multalin/cgi-bin/multalin.pl>), with the default parameters indicated on these websites.

Please replace the paragraphs at page 10 lines 18-27 with the following amended paragraphs.

The PFAM database (protein families database of alignments and hidden Markov models <http://www.sanger.ac.uk/Software/Pfam/>) is a large collection of alignments of protein sequences. Each PFAM makes it possible to visualise multiple alignments, view protein domains, evaluate distributions among organisms, gain access to other databases and visualise known protein structures.

COGs (clusters of orthologous groups of proteins <http://www.ncbi.nlm.nih.gov/COG/>) are obtained by comparing protein sequences derived from 43 fully sequenced genomes representing 30 major phylogenetic lines. Each COG is defined from at least three lines, making it possible to identify ancient conserved domains.

Please replace the paragraph at page 14 lines 15-22 with the following amended paragraph.

The present invention leads advantageously to the selection of mutations of the gene *lpd* (the wild sequence of which is known: <http://genolist.pasteur.fr/Colibri>) coding for the lipoamide dehydrogenase of the pyruvate dehydrogenase complex. In particular, the presence of a point mutation causing the replacement of alanine 55 by a valine has been identified. This enzyme is known to be responsible for the inhibition of the pyruvate dehydrogenase complex by NADH. This modified enzyme is also an object of the present invention.

Please replace the paragraph at page 16 lines 4-6 with the following amended paragraph.

- a region (lower-case letters) homologous to the sequence (4109007-4109087) of the gene *tpiA* (sequence 4108320 to 4109087), a reference sequence on the website <http://genolist.pasteur.fr/Colibri/>), and

Please replace the paragraph at page 17 lines 20-23 with the following amended paragraph.

- a region (lower-case letters) homologous to the sequence (952235-952315) of the gene *plfB* (sequence 950495 to 952777), a reference sequence on the website <http://genolist.pasteur.fr/Colibri/>), and

Please replace the paragraph at page 20 lines 17-19 with the following amended paragraph.

- a region (lower case letters) homologous to the sequence (1297263-1297343) of the gene *adhE* (sequence 1294669 to 1297344), a reference sequence on the site <http://genolist.pasteur.fr/Colibri/>), and

Please replace the paragraph at page23 lines 1-3 with the following amended paragraph.

- a region (lower case letters) homologous to the sequence (1725861-1725941) of the gene *gloA* (sequence 1725861 to 1726268), reference sequence on the website <http://genolist.pasteur.fr/Colibri/>), and

Please replace the paragraph at page24 lines 23-25 with the following amended paragraph.

- a region (lower case letters) homologous to the sequence (1486256-1486336) of the gene *aldA* (sequence 1486256 to 1487695), reference sequence on the website <http://genolist.pasteur.fr/Colibri/>), and

Please replace the paragraph at page26 lines 14-16 with the following amended paragraph.

- a region (lower case letters) homologous to the sequence (3752603-3752683) of the gene *aldB* (sequence from 3752603 to 3754141), reference sequence on the website <http://genolist.pasteur.fr/Colibri/>), and

Please replace the paragraph at page 31 lines 4-6 with the following amended paragraph.

- a region (lower case letters) homologous to the sequence (4135512 to 4135592) of the gene *gldA* (sequence 4135512 to 4136615), reference sequence on the website <http://genolist.pasteur.fr/Colibri/>), and

Please replace the paragraph at page 34 lines 5-7 with the following amended paragraph.

- a region (lower case letters) homologous to the sequence (1930817 to 4) of the gene *edd* (sequence 1930817 to 1932628), reference sequence on the website <http://genolist.pasteur.fr/Colibri/>), and